CRF Errors Corrected by the STIC Systems Branch

ENTERED

Serial Number: 09/720,451

CRF Processing Date: 8/15/2001
Edited by: _____
Verified by: _____ (STIC staf

☐ Changed a file from non-ASCII to ASCII.

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☑ Corrected an obvious error in the response, specifically:
  <157> response

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other: _____
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

```
               RAW SEQUENCE LISTING              DATE: 08/15/2001
               PATENT APPLICATION:  US/09/720,451   TIME: 09:42:37

               Input Set : A:\Pto.amc
               Output Set: N:\CRF3\08132001\I720451.raw
```

```
     1  <110>  APPLICANT: Falco, Carl
     2         Famodu, Layo O.
     4  <120>  TITLE OF INVENTION: Tetrahydrofolate Metabolism Enzymes
     6  <130>  FILE REFERENCE: BB-1179
C-->  8  <140>  CURRENT APPLICATION NUMBER: US/09/720,451
C-->  9  <141>  CURRENT FILING DATE: 2001-06-26
    11  <150>  PRIOR APPLICATION NUMBER: 60/092,869
    12  <151>  PRIOR FILING DATE: 1998-07-15
    14  <160>  NUMBER OF SEQ ID NOS: 8
    16  <170>  SOFTWARE: Microsoft Office 97
    18  <210>  SEQ ID NO: 1
    19  <211>  LENGTH: 542
    20  <212>  TYPE: DNA
    21  <213>  ORGANISM: Zea mays
    23  <220>  FEATURE:
    24  <221>  NAME/KEY: unsure
    25  <222>  LOCATION: (363)
    27  <400>  SEQUENCE: 1
    28  gcacgagcat tagagcgcgc gcgccaagct cgtggtgagg ttttcgagat gaaggttatc  60
    29  gagaagatcc tggaggcggc gggggatggc cggacggcgt tctcgttcga gtacttccct 120
    30  cccaagacgg aggagggggt cgagaacctg ttcgagcgga tggaccgcat ggtggcgcac 180
    31  ggccccctcct tctgcgacat cacctggggc gccgggggat ccaccgctga ccttaccctc 240
    32  gaaatcgcca accgtatgca gaacatggtg tgtgtggaaa ccatgatgca cctgacatgt 300
    33  acaaacatgc cagtagagaa gattgaccat gccttggaaa ccatcaaatc caatgggatt 360
W-->  34  canaatgttt tggccctcag aggggattct ccacatgggc aagacaaatt tgtgcaagtt 420
    35  gaaggcggat ttgcttgtgc tcttgatttg gtgacacata ttatagccaa gtacggtgaa 480
    36  ttattttggc atactgttac tggttatcag aagcacacct tgagcgatac atgcgaggga 540
    37  gg                                                               542
    39  <210>  SEQ ID NO: 2
    40  <211>  LENGTH: 164
    41  <212>  TYPE: PRT
    42  <213>  ORGANISM: Zea mays
    44  <220>  FEATURE:
    45  <221>  NAME/KEY: UNSURE
    46  <222>  LOCATION: (105)
    48  <400>  SEQUENCE: 2
    49  Met Lys Val Ile Glu Lys Ile Leu Glu Ala Ala Gly Asp Gly Arg Thr
    50   1               5                  10                  15
    52  Ala Phe Ser Phe Glu Tyr Phe Pro Pro Lys Thr Glu Glu Gly Val Glu
    53                  20                  25                  30
    55  Asn Leu Phe Glu Arg Met Asp Arg Met Val Ala His Gly Pro Ser Phe
    56              35                  40                  45
    58  Cys Asp Ile Thr Trp Gly Ala Gly Gly Ser Thr Ala Asp Leu Thr Leu
    59      50                  55                  60
    61  Glu Ile Ala Asn Arg Met Gln Asn Met Val Cys Val Glu Thr Met Met
    62  65                  70                  75                  80
    64  His Leu Thr Cys Thr Asn Met Pro Val Glu Lys Ile Asp His Ala Leu
```

RAW SEQUENCE LISTING   DATE: 08/15/2001
PATENT APPLICATION: **US/09/720,451**   TIME: 09:42:37

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\08132001\I720451.raw**

```
65                  85                  90                  95
67 Glu Thr Ile Lys Ser Asn Gly Ile Xaa Asn Val Leu Ala Leu Arg Gly
68                  100                 105                 110
70 Asp Ser Pro His Gly Gln Asp Lys Phe Val Gln Val Glu Gly Gly Phe
71             115                 120                 125
73 Ala Cys Ala Leu Asp Leu Val Thr His Ile Ile Ala Lys Tyr Gly Glu
74        130                 135                 140
76 Leu Phe Trp His Thr Val Thr Gly Tyr Gln Lys His Thr Leu Ser Asp
77 145                 150                 155                 160
79 Thr Cys Glu Gly
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 591
84 <212> TYPE: DNA
85 <213> ORGANISM: Oryza sativa
87 <220> FEATURE:
88 <221> NAME/KEY: unsure
89 <222> LOCATION: (535)
91 <220> FEATURE:
92 <221> NAME/KEY: unsure
93 <222> LOCATION: (548)
95 <220> FEATURE:
96 <221> NAME/KEY: unsure
97 <222> LOCATION: (554)
99 <220> FEATURE:
100 <221> NAME/KEY: unsure
101 <222> LOCATION: (557)
103 <220> FEATURE:
104 <221> NAME/KEY: unsure
105 <222> LOCATION: (561)
107 <220> FEATURE:
108 <221> NAME/KEY: unsure
109 <222> LOCATION: (591)
111 <400> SEQUENCE: 3
112 tctaccttac cttacctcac ctcacaaggg acaaagataa aaaatgaaga tcattgagaa   60
113 aattcacgca gcctcggctg atccaaacag ggtggtgttc tcatttgagt tcttcccgcc  120
114 caagactgag gatggggtgg acaatctgtt tgagaggatg gaccgcatgg tggtgcacaa  180
115 cccctcgttt tgcgacatca cttgggggtgc tggagggaca acggctgatc ttacattgga  240
116 aattgccaac aagatgcaga acattgtctg tgtggagacc atgatgcacc tcacctgcac  300
117 caacatgcct gttgagaaga ttgaccatgc tctccacacc atcaagtcca atggcctcca  360
118 aaatgtgctt gcacttcgag gtgatccacc gcatggtcag gacaaattcg tccagtcgaa  420
119 ggcggtttcc tgtgcacgcg acttggtgca acatatcaga ctaaatatgg tgacacttgg  480
120 ataagtcctg gtatcagagc acaccggatg tatagaatga tggttggcac acagnggtac  540
121 aaatatcnct actnaanaca ngttatctgg acattcgatg caccattttt n            591
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 408
125 <212> TYPE: PRT
126 <213> ORGANISM: Oryza sativa
128 <400> SEQUENCE: 4
129 Ala Arg Val Ile Val Thr Gln Leu Phe Tyr Asp Thr Asp Ile Phe Leu
```

```
130   1               5                 10                  15
132 Lys Phe Val Asn Asp Cys Arg Gln Ile Gly Ile Thr Cys Pro Ile Val
133            20                25                30
135 Pro Gly Ile Met Pro Ile Asn Asn Tyr Lys Gly Phe Ile Arg Met Thr
136            35                40                45
138 Gly Phe Cys Lys Thr Lys Ile Pro Ala Asp Ile Met Ala Ala Leu Glu
139      50                55                60
141 Pro Ile Lys Asp Asn Glu Glu Ala Val Lys Ala Tyr Gly Ile His Leu
142  65                70                75                80
144 Gly Thr Glu Met Cys Lys Lys Ile Leu Ala His Gly Ile Lys Thr Leu
145            85                90                95
147 His Leu Tyr Thr Leu Asn Met Glu Lys Ser Ala Leu Ala Ile Leu Met
148            100               105               110
150 Asn Leu Gly Leu Ile Glu Glu Ser Lys Val Ser Arg Ser Leu Pro Trp
151            115               120               125
153 Arg Arg Pro Ala Asn Val Phe Arg Val Lys Glu Asp Val Arg Pro Ile
154      130               135               140
156 Phe Trp Ala Asn Arg Pro Lys Ser Tyr Ile Ser Arg Thr Ile Gly Trp
157 145               150               155               160
159 Asp Gln Tyr Pro His Gly Arg Trp Gly Asp Ser Cys Asn Pro Ser Tyr
160            165               170               175
162 Gly Ala Leu Ser Asp Tyr Gln Phe Met Arg Pro Arg Ala Arg Asp Lys
163            180               185               190
165 Lys Leu Val Glu Glu Trp Ala Val Pro Leu Lys Ser Val Glu Asp Ile
166            195               200               205
168 Tyr Glu Arg Phe Arg Leu Tyr Cys Leu Gly Lys Leu Arg Ser Asn Pro
169      210               215               220
171 Trp Ser Glu Leu Asp Gly Leu Gln Pro Glu Thr Lys Ile Ile Asn Glu
172 225               230               235               240
174 Gln Leu Glu Lys Ile Asn Thr Lys Gly Phe Leu Thr Ile Asn Ser Gln
175            245               250               255
177 Pro Ala Val Asn Gly Glu Lys Ser Asp Ser Pro Thr Val Gly Trp Gly
178            260               265               270
180 Gly Pro Gly Gly Tyr Val Tyr Gln Lys Ala Tyr Val Glu Phe Phe Cys
181      275               280               285
183 Ser Lys Glu Lys Leu Asp Ala Leu Val Asp Lys Cys Lys Asp Arg Thr
184      290               295               300
186 Ser Leu Thr Tyr Met Ala Val Asn Lys Asp Gly Ser Trp Lys Ser Asn
187 305               310               315               320
189 Val Gly Gln Thr Asp Val Asn Ala Val Thr Trp Gly Val Phe Pro Ala
190            325               330               335
192 Lys Glu Ile Ile Gln Pro Thr Ile Val Asp Pro Val Ser Phe Asn Val
193            340               345               350
195 Trp Lys Asp Glu Ala Phe Glu Ile Trp Ser Arg Gly Trp Ala Ser Leu
196      355               360               365
198 Tyr Pro Glu Asp Glu Ala Ser Arg Lys Leu Val Glu Glu Val Gly Gly
199      370               375               380
201 Ser His Phe Leu Val Ser Leu Val Asp Asn Asp Tyr Ile Asn Gly Asp
202 385               390               395               400
```

```
204 Leu Phe Ala Val Phe Ala Asp Phe
205                 405
207 <210> SEQ ID NO: 5
208 <211> LENGTH: 558
209 <212> TYPE: DNA
210 <213> ORGANISM: Glycine max
212 <400> SEQUENCE: 5
213 tgattgtcac ccaattattt tatgatacgg atatattcct caaatttgtg aacgactgtc  60
214 gccaaattgg aataacgtgt cctattgtac ctggaattat gcccattaat aattacaagg 120
215 gctttatccg catgactggg ttttgcaaaa caaagatacc agctgacatt atggctgctt 180
216 tagagcctat caaggacaat gaagaagctg tcaaggctta tggaattcac ctgggaactg 240
217 aaatgtgcaa aaagatttta gctcatggaa ttaagacatt gcatctttat acactaaata 300
218 tggagaaatc tgcattggca atactaatga accttggcct aattgaagag tccaaagttt 360
219 ctaggtcctt accttggaga cgccctgcaa atgttttccg tgttaaagaa gatgtccgtc 420
220 caatcttttg ggcaaatcga ccaaaaagct acatatcaag gaccatagga tgggatcaat 480
221 acccacatgg gcgttggggt gattcctgta atccatcata tggtgcatta tctgattatc 540
222 agttcatgcg gccacgtg                                               558
224 <210> SEQ ID NO: 6
225 <211> LENGTH: 408
226 <212> TYPE: PRT
227 <213> ORGANISM: Glycine max
229 <400> SEQUENCE: 6
230 Ala Arg Val Ile Val Thr Gln Leu Phe Tyr Asp Thr Asp Ile Phe Leu
231  1               5               10                  15
233 Lys Phe Val Asn Asp Cys Arg Gln Ile Gly Ile Thr Cys Pro Ile Val
234             20              25                  30
236 Pro Gly Ile Met Pro Ile Asn Asn Tyr Lys Gly Phe Ile Arg Met Thr
237         35              40                  45
239 Gly Phe Cys Lys Thr Lys Ile Pro Ala Asp Ile Met Ala Ala Leu Glu
240     50              55                  60
242 Pro Ile Lys Asp Asn Glu Glu Ala Val Lys Ala Tyr Gly Ile His Leu
243  65              70                  75                  80
245 Gly Thr Glu Met Cys Lys Lys Ile Leu Ala His Gly Ile Lys Thr Leu
246             85              90                  95
248 His Leu Tyr Thr Leu Asn Met Glu Lys Ser Ala Leu Ala Ile Leu Met
249         100             105             110
251 Asn Leu Gly Leu Ile Glu Glu Ser Lys Val Ser Arg Ser Leu Pro Trp
252         115             120             125
254 Arg Arg Pro Ala Asn Val Phe Arg Val Lys Glu Asp Val Arg Pro Ile
255     130             135             140
257 Phe Trp Ala Asn Arg Pro Lys Ser Tyr Ile Ser Arg Thr Ile Gly Trp
258 145             150             155             160
260 Asp Gln Tyr Pro His Gly Arg Trp Gly Asp Ser Cys Asn Pro Ser Tyr
261             165             170             175
263 Gly Ala Leu Ser Asp Tyr Gln Phe Met Arg Pro Arg Ala Arg Asp Lys
264             180             185             190
266 Lys Leu Val Glu Glu Trp Ala Val Pro Leu Lys Ser Val Glu Asp Ile
267         195             200             205
269 Tyr Glu Arg Phe Arg Leu Tyr Cys Leu Gly Lys Leu Arg Ser Asn Pro
```

```
270      210                  215                  220
272 Trp Ser Glu Leu Asp Gly Leu Gln Pro Glu Thr Lys Ile Ile Asn Glu
273 225                  230              235                  240
275 Gln Leu Glu Lys Ile Asn Thr Lys Gly Phe Leu Thr Ile Asn Ser Gln
276                  245              250                  255
278 Pro Ala Val Asn Gly Glu Lys Ser Asp Ser Pro Thr Val Gly Trp Gly
279                  260              265                  270
281 Gly Pro Gly Gly Tyr Val Tyr Gln Lys Ala Tyr Val Glu Phe Phe Cys
282          275              280                  285
284 Ser Lys Glu Lys Leu Asp Ala Leu Val Asp Lys Cys Lys Asp Arg Thr
285          290              295                  300
287 Ser Leu Thr Tyr Met Ala Val Asn Lys Asp Gly Ser Trp Lys Ser Asn
288 305                  310              315                  320
290 Val Gly Gln Thr Asp Val Asn Ala Val Thr Trp Gly Val Phe Pro Ala
291                  325              330                  335
293 Lys Glu Ile Ile Gln Pro Thr Ile Val Asp Pro Val Ser Phe Asn Val
294                  340              345                  350
296 Trp Lys Asp Glu Ala Phe Glu Ile Trp Ser Arg Gly Trp Ala Ser Leu
297          355              360                  365
299 Tyr Pro Glu Asp Glu Ala Ser Arg Lys Leu Val Glu Glu Val Gly Gly
300      370              375                  380
302 Ser His Phe Leu Val Ser Leu Val Asp Asn Asp Tyr Ile Asn Gly Asp
303 385                  390              395                  400
305 Leu Phe Ala Val Phe Ala Asp Phe
306                  405
308 <210> SEQ ID NO: 7
309 <211> LENGTH: 451
310 <212> TYPE: DNA
311 <213> ORGANISM: Triticum aestivum
313 <220> FEATURE:
314 <221> NAME/KEY: unsure
315 <222> LOCATION: (25)
317 <220> FEATURE:
318 <221> NAME/KEY: unsure
319 <222> LOCATION: (115)
321 <220> FEATURE:
322 <221> NAME/KEY: unsure
323 <222> LOCATION: (120)
325 <220> FEATURE:
326 <221> NAME/KEY: unsure
327 <222> LOCATION: (176)
329 <220> FEATURE:
330 <221> NAME/KEY: unsure
331 <222> LOCATION: (347)
333 <220> FEATURE:
334 <221> NAME/KEY: unsure
335 <222> LOCATION: (371)
337 <220> FEATURE:
338 <221> NAME/KEY: unsure
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 08/15/2001
PATENT APPLICATION: **US/09/720,451**   TIME: 09:42:38

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\08132001\I720451.raw**

```
L:8  M:270 C: Current Application Number differs, Replaced Application Number
L:9  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:67 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:121 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:350 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:351 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:352 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:356 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:357 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:384 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:390 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
```

A Johnson

RAW SEQUENCE LISTING   DATE: 07/19/2001
PATENT APPLICATION: US/09/720,451   TIME: 12:29:05

Input Set : A:\BB-1179 Seq List.txt
Output Set: N:\CRF3\07192001\I720451.raw

Does Not Comply
Corrected Diskette Needed

```
      3 <110> APPLICANT: Falco, Carl
      4         Famodu, Layo O.
      6 <120> TITLE OF INVENTION: Tetrahydrofolate Metabolism Enzymes
      8 <130> FILE REFERENCE: BB-1179
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/720,451
C--> 11 <141> CURRENT FILING DATE: 2001-06-26
     13 <150> PRIOR APPLICATION NUMBER: 60/092,869
W--> 14 <151> PRIOR FILING DATE: July 15, 1998  1998-07-15
     16 <160> NUMBER OF SEQ ID NOS: 8
     18 <170> SOFTWARE: Microsoft Office 97
```

ERRORED SEQUENCES

```
    361 <210> SEQ ID NO: 8
    362 <211> LENGTH: 101
    363 <212> TYPE: PRT
    364 <213> ORGANISM: Triticum aestivum
    366 <220> FEATURE:
    367 <221> NAME/KEY: UNSURE
    368 <222> LOCATION: (25)..(26)
    370 <220> FEATURE:
    371 <221> NAME/KEY: UNSURE
    372 <222> LOCATION: (29)
    374 <220> FEATURE:
    375 <221> NAME/KEY: UNSURE
    376 <222> LOCATION: (31)
    378 <220> FEATURE:
    379 <221> NAME/KEY: UNSURE
    380 <222> LOCATION: (49)
    382 <400> SEQUENCE: 8
    383 Glu His Ile Lys Ala Lys Tyr Gly Asp Tyr Phe Gly Ile Thr Val Ala
    384  1               5               10                  15
W-> 386 Gly Tyr Pro Glu Ala His Pro Glu Xaa Xaa Ala Tyr Xaa Lys Xaa Leu
    387             20              25                  30
    389 Ala Tyr Leu Lys Arg Lys Val Asp Ala Gly Ala Asp Val Ile Ile Thr
    390         35              40                  45
W-> 392 Xaa Leu Phe Tyr Asp Thr Asp Ile Phe Leu Lys Phe Val Asn Asp Cys
    393     50              55                  60
    395 Arg Gln Ile Gly Ile Thr Cys Pro Ile Val Pro Gly Ile Met Pro Ile
    396 65              70                  75                  80
    398 Asn Asn Tyr Lys Gly Phe Val Arg Met Thr Gly Phe Cys Lys Thr Lys
    399             85                  90                  95
    401 Ile Pro Pro Glu Ile
    402             100
E-> 404 7
```

VERIFICATION SUMMARY   DATE: 07/19/2001
PATENT APPLICATION: **US/09/720,451**   TIME: 12:29:06

Input Set : **A:\BB-1179 Seq List.txt**
Output Set: **N:\CRF3\07192001\I720451.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Application Number
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14  M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:36  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:36  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:69  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:69  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:122 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:123 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:352 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:353 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:354 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:357 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:358 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:386 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:392 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:404 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
```